

SEQUENCE LISTING



<110> McCarthy, Sean A.

<120> NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> MNI-108CP2

<140> 09/263,022

<141> 1999-03-05

<150> 08/843,704

<151> 1997-04-16

<150> 08/842,898

<151> 1997-04-17

<150> 60/071,589

<151> 1998-01-15

<150> 09/009,802

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<223> 'n' at position 1146 may be any nucleotide

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Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala  
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ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc gcc ccg gct ctc 151  
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu  
25 30 35

agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199  
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val  
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a!

gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa	247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu	
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Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn	
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ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg	343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	
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aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata	391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
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Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
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Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
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Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
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Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
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Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
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Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
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Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
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cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg	823
Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
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gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac	871
Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
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agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa	919
Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
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315 320 325

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Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala  
330 335 340

gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggtagatgtg 1117  
Ala Leu Leu Gly Arg Glu Glu Ile  
345 350

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ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac atggttgtaa tatgcgactg 2257

cgaacactga actctacgcc actccacaaa tgatgttttc aggtgtcatg gactgttgcc 2317

accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
85 90 95

Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His  
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
 290 295 300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
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 gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc 96  
 Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
 20 25 30  
 aag ccc ggc ccg gct ctc agc tac ccg cag gag gag gcc acc ctc aat 144  
 Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45  
 gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa 192  
 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60  
 ttg cgc agc gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa 240  
 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80  
 gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat 288  
 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
 85 90 95  
 gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac 336  
 Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His  
 100 105 110  
 cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt 384  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
 115 120 125  
 tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc 432  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
 130 135 140

cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag 480  
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
145 150 155 160

ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg 528  
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
165 170 175

ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg 576  
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
180 185 190

ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt 624  
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
195 200 205

gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga 672  
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
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ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt 720  
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta 768  
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc 816  
Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc 864  
Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
275 280 285

gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc 912  
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ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag 960  
Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
305 310 315 320

ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag 1008  
Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu  
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 aagg atg gtg gcg gcc gtc ctg ctg ggg ctg agc tgg ctc tgc tct ccc 169  
     Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro  
     1                    5                    10                    15  
 ctg gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac 217  
 Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp  
                     20                    25                    30  
 ctg cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc 265  
 Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys  
                     35                    40                    45  
 aat acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt 313  
 Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys  
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 gct aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc 361  
 Ala Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys  
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 tgc cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat 409  
 Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp  
                     80                    85                    90                    95  
 gca acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat 457  
 Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His  
                     100                    105                    110  
 gca gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg 505  
 Ala Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg  
                     115                    120                    125  
 aag cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa 553  
 Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu  
                     130                    135                    140  
 agt tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt 601  
 Ser Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg  
                     145                    150                    155  
 cat ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc 649  
 His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val  
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 tgc tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc 697  
 Cys Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe  
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 cag cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc 745  
 Gln Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr  
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 agc aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag 793  
 Ser Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys  
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His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn  
35 40 45  
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala  
50 55 60  
Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys  
65 70 75 80  
Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala  
85 90 95  
Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala  
100 105 110  
Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys  
115 120 125  
Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser  
130 135 140  
Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His  
145 150 155 160  
Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys  
165 170 175  
Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln  
180 185 190  
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Gly	Ala	Leu	Val	Leu	Asp	Phe	Asn	Asn	Ile	Arg	Ser	Ser	Ala	Asp	Leu	
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cat	ggg	gcc	cgg	aag	ggc	tca	cag	tgc	ctg	tct	gac	acg	gac	tgc	aat	144
His	Gly	Ala	Arg	Lys	Gly	Ser	Gln	Cys	Leu	Ser	Asp	Thr	Asp	Cys	Asn	
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Thr	Arg	Lys	Phe	Cys	Leu	Gln	Pro	Arg	Asp	Glu	Lys	Pro	Phe	Cys	Ala	
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aca	tgt	cgt	ggg	ttg	cgg	agg	agg	tgc	cag	cga	gat	gcc	atg	tgc	tgc	240
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65				70					75					80		
cct	ggg	aca	ctc	tgt	gtg	aac	gat	ggt	tgt	act	acg	atg	gaa	gat	gca	288
Pro	Gly	Thr	Leu	Cys	Val	Asn	Asp	Val	Cys	Thr	Thr	Met	Glu	Asp	Ala	
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acc	cca	ata	tta	gaa	agg	cag	ctt	gat	gag	caa	gat	ggc	aca	cat	gca	336
Thr	Pro	Ile	Leu	Glu	Arg	Gln	Leu	Asp	Glu	Gln	Asp	Gly	Thr	His	Ala	
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gaa	gga	aca	act	ggg	cac	cca	gtc	cag	gaa	aac	caa	ccc	aaa	agg	aag	384
Glu	Gly	Thr	Thr	Gly	His	Pro	Val	Gln	Glu	Asn	Gln	Pro	Lys	Arg	Lys	
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cca	agt	att	aag	aaa	tca	caa	ggc	agg	aag	gga	caa	gag	gga	gaa	agt	432
Pro	Ser	Ile	Lys	Lys	Ser	Gln	Gly	Arg	Lys	Gly	Gln	Glu	Gly	Glu	Ser	
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tgt	ctg	aga	act	ttt	gac	tgt	ggc	cct	gga	ctt	tgc	tgt	gct	cgt	cat	480
Cys	Leu	Arg	Thr	Phe	Asp	Cys	Gly	Pro	Gly	Leu	Cys	Cys	Ala	Arg	His	
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Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	Leu	Glu	Gly	Gln	Val	Cys	
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Ser	Arg	Arg	Gly	His	Lys	Asp	Thr	Ala	Gln	Ala	Pro	Glu	Ile	Phe	Gln	
			180					185					190			
cgt	tgc	gac	tgt	ggc	cct	gga	cta	ctg	tgt	cga	agc	caa	ttg	acc	agc	624
Arg	Cys	Asp	Cys	Gly	Pro	Gly	Leu	Leu	Cys	Arg	Ser	Gln	Leu	Thr	Ser	
		195					200					205				
aat	cgg	cag	cat	gct	cga	tta	aga	gta	tgc	caa	aaa	ata	gaa	aag	cta	672
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Met Met Ala  
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ctg ggc gca gcg gga gct acc cgg gtc ttt gtc gcg atg gta gcg gcg 165  
Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met Val Ala Ala  
5 10 15  
gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc ttg aac tcg 213  
Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser  
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gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg ctg ggc ggc 261  
Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly  
40 45 50  
gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg gga atc ctg 309  
Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro Gly Ile Leu  
55 60 65  
tac ccg ggc ggg aat aag tac cag acc att gac aac tac cag ccg tac 357  
Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr Gln Pro Tyr  
70 75 80  
ccg tgc gca gag gac gag gag tgc ggc act gat gag tac tgc gct agt 405  
Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr Cys Ala Ser  
85 90 95  
ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc gcc tgc agg 453  
Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu Ala Cys Arg  
100 105 110 115  
aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc ccc ggg aat 501  
Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys Pro Gly Asn  
120 125 130  
tac tgc aaa aat gga ata tgt gtg tct tct gat caa aat cat ttc cga 549  
Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg  
135 140 145  
gga gaa att gag gaa acc atc act gaa agc ttt ggt aat gat cat agc 597  
Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser  
150 155 160  
acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca aaa atg tat 645  
Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr  
165 170 175

cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt 693  
His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys  
180 185 190 195

gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag atc tgt aaa 741  
Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys  
200 205 210

cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc 789  
Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly  
215 220 225

tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg 837  
Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu  
230 235 240

tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat tct tct agg 885  
Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg  
245 250 255

ctt cac act tgt cag aga cac taaaccagct atccaaatgc agtgaactcc 936  
Leu His Thr Cys Gln Arg His  
260 265

ttttatataa tagatgctat gaaaaccttt tatgaccttc atcaactcaa tccctaaggat 996

atacaagttc tgtggtttca gttaagcatt ccaataacac cttccaaaaa cctggagtgt 1056

aagagctttg tttctttatg gaactcccct gtgattgcag taaattactg tattgtaaat 1116

tctcagtgtg gcacttacct gtaaatagcaa tgaaactttt aattatTTTT ctaaagggtgc 1176

tgcaactgcct attttctctc ttgttatgta aatTTTTgta cacattgatt gttatcttga 1236

ctgacaaata ttctatattg aactgaagta aatcatttca gcttatagtt cttaaaagca 1296

taacccttta cccatttaa ttctagagtc tagaacgcaa ggatctcttg gaatgacaaa 1356

tgataggtac ctaaaatgta acatgaaaat actagcttat tttctgaaat gtactatctt 1416

aatgcttaaa ttatatttcc ctttaggctg tgatagtttt tgaataaaaa ttttaacattt 1476

aatatcatga aatgttataa gtagacataa aaaaaaaaaa aaaaaaaaaa gggcgggccgc 1536

<210> 8

<211> 266.

<212> PRT

<213> Homo sapiens

<400> 8

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Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr  
20 25 30

Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro  
35 40 45

Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro  
50 55 60

Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr  
65 70 75 80

Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr  
85 90 95

Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu  
100 105 110

Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys  
115 120 125

Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn  
130 135 140

His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn  
145 150 155 160

Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser  
165 170 175

Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser  
180 185 190

Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys  
195 200 205

Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg  
210 215 220

Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
225 230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn  
245 250 255

Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 9  
<211> 798  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(798)

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Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met  
1 5 10 15

gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc 96  
Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr  
20 25 30

ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg	144
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro	
35 40 45	
ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg	192
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro	
50 55 60	
gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac	240
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr	
65 70 75 80	
cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac	288
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr	
85 90 95	
tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc	336
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu	
100 105 110	
gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc	384
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys	
115 120 125	
ccc ggg aat tac tgc aaa aat gga ata tgt gtg tct tct gat caa aat	432
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn	
130 135 140	
cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat	480
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn	
145 150 155 160	
gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca	528
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser	
165 170 175	
aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca	576
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser	
180 185 190	
tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag	624
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys	
195 200 205	
atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg	672
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg	
210 215 220	
aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga	720
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly	
225 230 235 240	
gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat	768
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn	
245 250 255	
tct tct agg ctt cac act tgt cag aga cac	798
Ser Ser Arg Leu His Thr Cys Gln Arg His	
260 265	

<210> 10  
<211> 702  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(537)

<400> 10  
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48  
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly  
1 5 10 15  
tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96  
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg  
20 25 30  
gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144  
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile  
35 40 45  
cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192  
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly  
50 55 60  
act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240  
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu  
65 70 75 80  
gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288  
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys  
85 90 95  
ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336  
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly  
100 105 110  
ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384  
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu  
115 120 125  
cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432  
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly  
130 135 140  
ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480  
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
145 150 155 160  
gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528  
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys  
165 170 175  
cag aaa att tgatcacat tgaggaacat catcaattgc agactgtgaa 577  
Gln Lys Ile  
gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637  
taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg 697

gccgc

<210> 11  
<211> 179  
<212> PRT  
<213> Homo sapiens

<400> 11  
 Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly  
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 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg  
                   20                  25                  30  
 Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile  
                   35                  40                  45  
 Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly  
                   50                  55                  60  
 Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu  
   65                  70                  75                  80  
 Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys  
                   85                  90                  95  
 Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly  
                   100                  105                  110  
 Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu  
                   115                  120                  125  
 His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly  
   130                  135                  140  
 Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 145                  150                  155                  160  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys  
                   165                  170                  175  
 Gln Lys Ile

<210> 12  
<211> 537  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(537)

<400> 12  
 gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48  
 Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly  
   1                  5                  10                  15







aaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc

<210> 14  
<211> 242  
<212> PRT  
<213> Homo sapiens

<400> 14  
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val  
1 5 10 15  
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro  
20 25 30  
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu  
35 40 45  
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu  
50 55 60  
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly  
65 70 75 80  
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly  
85 90 95  
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn  
100 105 110  
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln  
115 120 125  
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu  
130 135 140  
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His  
145 150 155 160  
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg  
165 170 175  
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu  
180 185 190  
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr  
195 200 205  
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg  
210 215 220  
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg  
225 230 235 240  
Gln Leu

<210> 15  
<211> 726

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(726)

<400> 15

atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg cat ctg ctg gtc	48
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val	
1 5 10 15	
ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct	96
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro	
20 25 30	
atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc	144
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu	
35 40 45	
cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg	192
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu	
50 55 60	
ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc	240
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly	
65 70 75 80	
ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg	288
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly	
85 90 95	
aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac	336
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn	
100 105 110	
aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa	384
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln	
115 120 125	
cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag	432
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu	
130 135 140	
gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac	480
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His	
145 150 155 160	
aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg	528
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg	
165 170 175	
cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag	576
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu	
180 185 190	
aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc	624
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr	
195 200 205	

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg	672
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg	
210 215 220	

ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg	720
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg	
225 230 235 240	

cag ctg	726
Gln Leu	

<210> 16  
 <211> 2380  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (109)..(1155)

<400> 26	
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gctcagcttt gttcattcga attgggcggc ggccagcgcg gaacaaac atg cag cgg	117
	Met Gln Arg
	1

ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act	165
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr	
5 10 15	

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc	213
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly	
20 25 30 35	

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt	261
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe	
40 45 50	

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt	309
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser	
55 60 65	

gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct	357
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Thr Ser Ser	
70 75 80	

gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc	405
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser	
85 90 95	

acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt	453
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val	
100 105 110 115	

cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca	501
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr	
120 125 130	

gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt 549  
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys  
135 140 145

atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc 597  
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser  
150 155 160

ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc 645  
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr  
165 170 175

cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc 693  
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys  
180 185 190 195

acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag 741  
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln  
200 205 210

agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg 789  
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu  
215 220 225

ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac 837  
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp  
230 235 240

ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa 885  
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu  
245 250 255

gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca 933  
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro  
260 265 270 275

cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc 981  
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser  
280 285 290

cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag 1029  
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu  
295 300 305

tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac 1077  
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp  
310 315 320

ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct 1125  
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro  
325 330 335

gtg gag tca cta ggc gga gag gag gag att taggccaga cccagctgag 1175  
Val Glu Ser Leu Gly Gly Glu Glu Glu Ile  
340 345

tcaactggtag atgtgcaata gaaatggcta atttatcttc ccaggagtgt cccaagtgt 1235

ggaatggccg cagctccttc ccagtagctt ttcctctggc ttgacaaggt acagtgcagt 1295

acatttcttc cagccgcctt gottctctga cttgggaaag acaggcatgg cgggtaaggg 1355

cagcggtag tcgtccctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag 1415  
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 acagggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgctttt 1535  
 gtcttgcgcc gctcccatgg gctgaggcag tggctacaca agagctatgc tgctctgtgg 1595  
 cctcccatat attcatccct gtgtttcagc tcctacctca ctgtcagcac agcccttcat 1655  
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 gccccatgct ctctctctca accccatacc agcctctgtg ccagcgacag tccttccaaa 1775  
 tggagggagt gaaatccttt ggtttaatta ttttctcctt caaggcacgc ctgccactaa 1835  
 ggtcaggctg acttgcatgt ccctctaacg ttcgtagcag tgtggtggac actgtcttcc 1895  
 accgactgct tcaatacctc tgaagccag tgctcggagt gcagttcgtg taaattaatt 1955  
 tgcaggaagt atacttggct aattgtaggg ctaggattgt gaatgaaatt tgcaaagtcg 2015  
 cttagcaaca atggaaagcc tttctcagtc acaccgagaa gtcacaacca agccaggttg 2075  
 tgtagagtac agctgtgaca tacagacaga agaaggctgg gctggatgac aggctcaga 2135  
 tgacggtttc aggtgccagg aactattacc attctgtatc tatccagagt tattaataatt 2195  
 gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2255  
 acaaacatgt ggcctcaaa gatcatgcac aaaccactac tctttgctaa ttcttggact 2315  
 tttctctttg attttcaata aatacaaate cccttcatgc aaaaaaaaaa aaaaagggcg 2375  
 gccgc 2380

<210> 17  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Met Gln Arg Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala  
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 Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala  
 20 25 30  
 Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45  
 Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60  
 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80  
 Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn  
 85 90 95

Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His  
100 105 110

Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe  
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser  
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln  
145 150 155 160

Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met  
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp  
180 185 190

Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys  
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240

Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu  
245 250 255

Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe  
275 280 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala  
290 295 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu  
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly  
325 330 335

Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile  
340 345

- <210> 18
- <211> 1047
- <212> DNA
- <213> Homo sapiens
  
- <220>
- <221> CDS
- <222> (1)..(1047)

<400> 18  
atg cag cgg ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg 48  
Met Gln Arg Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala  
1 5 10 15

gtc ccc act gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg 96  
Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala  
20 25 30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat 144  
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
35 40 45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa 192  
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
50 55 60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa 240  
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
65 70 75 80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat 288  
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn  
85 90 95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac 336  
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His  
100 105 110

cag gaa gtt cac aag ata acc aac aac cag agt gga cag gtg gtc ttt 384  
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe  
115 120 125

tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc 432  
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser  
130 135 140

cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag 480  
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln  
145 150 155 160

ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg 528  
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met  
165 170 175

cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg 576  
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp  
180 185 190

ggt cac tgc acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt 624  
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys  
195 200 205

gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga 672  
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg  
210 215 220

ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc 720  
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
225 230 235 240





gcgggaccaa ggaggtgcgg ggcaagaagg aacggaagcg gtgcatcca cagggctggg 420  
ttttcttgca ccttgggtca cgctccttg gcgagaaagc gcctcgatt tgattgcttc 480  
cagttattgc agaacttctt gtctgtgtgg agaagcgggt ctgcttggg ttccgctaata 540  
ttctgtcctg aggcgtgaga ctgagttcat agggctctgg gtccccgaac caggaagggt 600  
tgaggaaca caatctgcaa gccccgcga cccaagtgag gggccccgtg ttggggctct 660  
ccctcccttt gcattcccac ccctccgggc tttgcgtctt cctggggacc c cct cgc 717  
Pro Arg  
1  
cgg gag atg gcc gcg ttg atg cgg agc aag gat tcg tcc tgc tgc ctg 765  
Arg Glu Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu  
5 10 15  
ctc cta ctg gcc gcg gtg ctg atg gtg gag agc tca cag atc ggc agt 813  
Leu Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
20 25 30  
tcg cgg gcc aaa ctc aac tcc atc aag tcc tct ctg ggc ggg gag acg 861  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu Thr  
35 40 45 50  
cct ggt cag gcc gcc aat cga tct gcg ggc atg tac caa gga ctg gca 909  
Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly Leu Ala  
55 60 65  
ttc ggc ggc agt aag aag ggc aaa aac ctg ggg cag gcc tac cct tgt 957  
Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala Tyr Pro Cys  
70 75 80  
agc agt gat aag gag tgt gaa gtt ggg agg tat tgc cac agt ccc cac 1005  
Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys His Ser Pro His  
85 90 95  
caa gga tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc 1053  
Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys  
100 105 110  
cac cga gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc 1101  
His Arg Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile  
115 120 125 130  
tgt atc cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg 1149  
Cys Ile Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu  
135 140 145  
gat ggt act cgg cac aga gat cga aac cac ggt cat tac tca aac cat 1197  
Asp Gly Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His  
150 155 160  
gac ttg gga tgg cag aat cta gga aga cca cac act aag atg tca cat 1245  
Asp Leu Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His  
165 170 175  
ata aaa ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att 1293  
Ile Lys Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile  
180 185 190

gaa ggg ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca 1341  
Glu Gly Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro  
195 200 205 210

gtg ctc cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct 1389  
Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser  
215 220 225

cat ggg ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct 1437  
His Gly Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser  
230 235 240

tgc aaa gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat 1485  
Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His  
245 250 255

gtg tgt cag aaa att tgatcacat tgaggaacat catcaattgc agactgtgaa 1540  
Val Cys Gln Lys Ile  
260

gttgtgtatt taatgcatta tagcatgggtg gaaaataagg ttcagatgca gaagaatggc 1600

taaaataaga aacgtgataa gaatatagat gatcacaaaa agggagaaaag aaaacatgaa 1660

ctgaatagat tagaatgggt gacaaatgca gtgcagccag tgtttccatt atgcaacttg 1720

tctatgtaaa taatgtacac atttgtggaa aatgctatta ttaagagaac aagcacacag 1780

tggaaattac tgatgagtag catgtgactt tccaagagtt taggttgtgc tggaggagag 1840

gtttccttca gattgctgat tgcttataca aataacctac atgccagatt tctattcaac 1900

gttagagttt aacaaaatac tctagaata acttggtata caataggttc taaaataaaa 1960

attgctaaac aagaaatgaa aacatggagc attgttaatt tacaacagaa aattaccttt 2020

tgatttgtaa cactacttct gctgttcaat caagagtctt ggtagataag aaaaaaatca 2080

gtcaatattt ccaaataatt gcaaaataat ggccagttgt ttaggaaggc ctttaggaag 2140

acaataaat aacaacaaa cagccacaaa tacttttttt tcaaaatttt agttttacct 2200

gtaattaata agaactgata caagacaaaa acagttcctt cagattctac ggaatgacag 2260

tatatctctc tttatcctat gtgattcctg ctctgaatgc attatatttt ccaaagtata 2320

cccataaatt gtgactagta aaatacttac acagagcaga attttcacag atggcaaaaa 2380

aatttaaaga tgtccaatat atgtgggaaa agagctaaca gagagatcat tatttcttaa 2440

agattggcca taacctgtat tttgatagaa ttagattgggt aaatacatgt attcatacat 2500

actctgtggt aatagagact tgagctggat ctgtactgca ctggagtaag caagaaaatt 2560

gggaaaactt tttcgtttgt tcaggttttg gcaacacata gatcatatgt ctgaggcaca 2620

agttggctgt tcacttttga aaccagggga tgcacagtct aatgaatat ctgcatggga 2680

tttgatcat aatatttact atgcagatga attcagtgtg aggtcctgtg tccgtactat 2740

cctcaaatta tttatTTTTat agtgctgaga tcctcaaata atctcaattt caggaggttt 2800  
 cacaaaatgg actcctgaag tagacagagt agtgaggttt cattgccctc tataagcttc 2860  
 tgactagcca atggcatcat ccaattttct tcccaaacct ctgcagcatc tgctttattg 2920  
 ccaaagggtt agtttcgggtt ttctgcagcc attgcgggta aaaaatataa gtaggataac 2980  
 ttgtaaaacc tgcataattgc taatctatag acaccacagt ttctaaattc tttgaaacca 3040  
 ctttactact ttttttaaac ttaactcagt tctaaatact ttgtctggag cacaaaacaa 3100  
 taaaagggta tcttatagtt gtgactttaa actttttagtag accacaattc actttttagt 3160  
 tttctttttac ttaaattcca tctgcagtct caaatttaag ttctcccagt agagattgag 3220  
 tttgagcctg tatatctatt aaaaatttca acttcccaca tatatttact aagatgatta 3280  
 agacttacat tttctgcaca ggtctgcaaa aacaaaaatt ataaactagt ccatccaaga 3340  
 accaaagttt gtataaacag gttgctataa gcttggtgaa atgaaaatgg aacatttcaa 3400  
 tcaaacattt cctatataac aattattata tttacaattt ggtttctgca atatttttct 3460  
 tatgtccacc cttttaaaaa ttattatttg aagtaattta tttacaggaa atgttaatga 3520  
 gatgtatttt cttatagaga tatttcttac agaaagcttt gtagcagaat atatttgcag 3580  
 ctattgactt tgtaatttag gaaaaatgta taataagata aaatctatta aatttttctc 3640  
 ctctaaaaac tgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc ggccgc 3696

<210> 21  
 <211> 263  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Pro Arg Arg Glu Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys  
 1 5 10 15  
 Cys Leu Leu Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile  
 20 25 30  
 Gly Ser Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly  
 35 40 45  
 Glu Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala Tyr  
 65 70 75 80  
 Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys His Ser  
 85 90 95  
 Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys  
 100 105 110

Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn  
 115 120 125

Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro  
 130 135 140

Ala Leu Asp Gly Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser  
 145 150 155 160

Asn His Asp Leu Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met  
 165 170 175

Ser His Ile Lys Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp  
 180 185 190

Cys Ile Glu Gly Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys  
 195 200 205

Lys Pro Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys  
 210 215 220

Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly  
 225 230 235 240

Leu Ser Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg  
 245 250 255

Leu His Val Cys Gln Lys Ile  
 260

<210> 22  
 <211> 789  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(789)

<400> 22  
 cct cgc cgg gag atg gcc gcg ttg atg cgg agc aag gat tcg tcc tgc 48  
 Pro Arg Arg Glu Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys  
 1 5 10 15

tgc ctg ctc cta ctg gcc gcg gtg ctg atg gtg gag agc tca cag atc 96  
 Cys Leu Leu Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile  
 20 25 30

ggc agt tcg cgg gcc aaa ctc aac tcc atc aag tcc tct ctg ggc ggg 144  
 Gly Ser Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly  
 35 40 45

gag acg cct ggt cag gcc gcc aat cga tct gcg ggc atg tac caa gga 192  
 Glu Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60

ctg gca ttc ggc ggc agt aag aag ggc aaa aac ctg ggg cag gcc tac 240  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala Tyr  
 65 70 75 80

cct tgt agc agt gat aag gag tgt gaa gtt ggg agg tat tgc cac agt 288  
 Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys His Ser  
 85 90 95

ccc cac caa gga tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag 336  
 Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys  
 100 105 110

cgc tgc cac cga gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat 384  
 Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn  
 115 120 125

ggc atc tgt atc cca gtt act gaa agc atc tta acc cct cac atc ccg 432  
 Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro  
 130 135 140

gct ctg gat ggt act cgg cac aga gat cga aac cac ggt cat tac tca 480  
 Ala Leu Asp Gly Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser  
 145 150 155 160

aac cat gac ttg gga tgg cag aat cta gga aga cca cac act aag atg 528  
 Asn His Asp Leu Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met  
 165 170 175

tca cat ata aaa ggg cat gaa gga gac ccc tgc cta cga tca tca gac 576  
 Ser His Ile Lys Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp  
 180 185 190

tgc att gaa ggg ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc 624  
 Cys Ile Glu Gly Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys  
 195 200 205

aaa cca gtg ctc cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag 672  
 Lys Pro Val Leu His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys  
 210 215 220

ggg tct cat ggg ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc 720  
 Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly  
 225 230 235 240

ctg tct tgc aaa gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga 768  
 Leu Ser Cys Lys Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg  
 245 250 255

ctc cat gtg tgt cag aaa att 789  
 Leu His Val Cys Gln Lys Ile  
 260

<210> 23

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus sequence

<220>

<223> Xaa's at positions

2, 3, 5, 6, 8-12, 14-26, 28, 29, 31-36, 38-42, 45-48, and

50-53 may be any amino acid

<220>

<223> Xaa's at postions 22-26 may be absent

<400> 23

Cys	Xaa	Xaa	Asp	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa
1				5					10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa
			20					25					30		

Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Cys	Xaa	Xaa	Xaa	Xaa
			35					40					45		

Cys	Xaa	Xaa	Xaa	Xaa	Cys
	50				

<210> 24

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus sequence

<220>

<223> Xaa's at positions 2, 5, 8, 9, 11, 14-23, 25, 27-30, 32, 33, 35-53, 60, 62, 63, 65, 68, 70, 71, 73-96, 98, 100, 101, 104, and 106-122 may be any amino acid

<220>

<223> Xaa's at positions 22, 23, 51-58, 89-96 and 116-122 may be absent

<400> 24

Cys	Xaa	Xaa	Xaa	Xaa	Asp	Cys	Xaa	Xaa	Gly	Xaa	Cys	Cys	Xaa	Xaa	Xaa
1					5				10					15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Gly	Xaa
			20					25						30	

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35						40					45		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys	Xaa	Xaa	Pro
		50						55				60			

Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70					75					80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85						90					95

Cys	Xaa	Cys	Xaa	Xaa	Gly	Leu	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105						110	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
115 120

<210> 25  
<211> 87  
<212> PRT  
<213> Homo sapiens

<400> 25  
Ile Asn Leu Glu Asn Gly Glu Leu Cys Met Asn Ser Ala Gln Cys Lys  
1 5 10 15  
Ser Asn Cys Cys Gln His Ser Ser Ala Leu Gly Leu Ala Arg Cys Thr  
20 25 30  
Ser Met Ala Ser Glu Asn Ser Glu Cys Ser Val Lys Thr Leu Tyr Gly  
35 40 45  
Ile Tyr Tyr Lys Cys Pro Cys Glu Arg Gly Leu Thr Cys Glu Gly Asp  
50 55 60  
Lys Thr Ile Val Gly Ser Ile Thr Asn Thr Asn Phe Gly Ile Cys His  
65 70 75 80  
Asp Ala Gly Arg Ser Lys Gln  
85

<210> 26  
<211> 835  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (57)..(746)

<400> 25  
gaattcggca cgaggcagaa ggcgcgaatg aaggcaaagc ctcccacca cctgca atg 59  
Met  
1  
tgt cga ctg agg gtc ttg ctg ctg ctg ctc ccc ttg gcc ttc gtg tcc 107  
Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val Ser  
5 10 15  
tcc tct gct ctc ccc atc cat gat gtc gac tct cag cag aac acc tcc 155  
Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr Ser  
20 25 30  
ggg ttc ctg ggc ctt cag agg ctt ctc caa agc ttt agt cga ctg ttc 203  
Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu Phe  
35 40 45  
cta aaa aat gac ctg cta cga gac ctg gac aac ttc ttc tcc tcc ccc 251  
Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser Pro  
50 55 60 65



atg gac ttc cga gac ctt cct agg aac ttc cat cag gaa gag aac cag 299  
Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn Gln  
70 75 80

gag cac aga atg ggc aac cat acc ctc tcc agc cac cta cag ata gac 347  
Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile Asp  
85 90 95

aag gtg act gac aac cag aca ggg gag gtg cac atc tcg gag aaa gtc 395  
Lys Val Thr Asp Asn Gln Thr Gly Glu Val His Ile Ser Glu Lys Val  
100 105 110

gag gcc tcc att gag cca gaa cgg aac ccg gaa ggg gac tgg aag gtt 443  
Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys Val  
115 120 125

ccc aaa gta gaa gca aaa gag ccc ccg gtg cct gtg cag aag gtc acc 491  
Pro Lys Val Glu Ala Lys Glu Pro Pro Val Pro Val Gln Lys Val Thr  
130 135 140 145

gac agc ttg cac cca gag ccc cgg cag gtg gct ttc tgg atc atg aag 539  
Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met Lys  
150 155 160

atg cca agg cgg agg acc cag ccc gat gtc cag gat gga ggc cgc tgg 587  
Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg Trp  
165 170 175

ctc ata gaa aag cga cat cgc atg cag gcc atc cgg gat ggg ctc cgt 635  
Leu Ile Glu Lys Arg His Arg Met Gln Ala Ile Arg Asp Gly Leu Arg  
180 185 190

gga ggc gcc cgt gag gac agc ctg gag gat ggg gtc cat atc ccc caa 683  
Gly Gly Ala Arg Glu Asp Ser Leu Glu Asp Gly Val His Ile Pro Gln  
195 200 205

cac gcc aag ctg cct gtc aga aag aca cac ttt ctc tac atc ctc agg 731  
His Ala Lys Leu Pro Val Arg Lys Thr His Phe Leu Tyr Ile Leu Arg  
210 215 220 225

cca tcc caa cag ctg taagtgggga ccagatgtcc cacaccctac cccaacacca 786  
Pro Ser Gln Gln Leu  
230

tatggaaata aaggttttct tacatctaaa aaaaaaaaaa aaaaaaaaaa 835

<210> 27

<211> 230

<212> PRT

<213> Mus musculus

<400> 27

Met Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val  
1 5 10 15

Ser Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr  
20 25 30

Ser Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu  
35 40 45

Phe Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser  
 50 55 60

Pro Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn  
 65 70 75 80

Gln Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile  
 85 90 95

Asp Lys Val Thr Asp Asn Gln Thr Gly Glu Val His Ile Ser Glu Lys  
 100 105 110

Val Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys  
 115 120 125

Val Pro Lys Val Glu Ala Lys Glu Pro Pro Val Pro Val Gln Lys Val  
 130 135 140

Thr Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met  
 145 150 155 160

Lys Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg  
 165 170 175

Trp Leu Ile Glu Lys Arg His Arg Met Gln Ala Ile Arg Asp Gly Leu  
 180 185 190

Arg Gly Gly Ala Arg Glu Asp Ser Leu Glu Asp Gly Val His Ile Pro  
 195 200 205

Gln His Ala Lys Leu Pro Val Arg Lys Thr His Phe Leu Tyr Ile Leu  
 210 215 220

Arg Pro Ser Gln Gln Leu  
 225 230

<210> 28  
 <211> 690  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(690)

<400> 28  
 atg tgt cga ctg agg gtc ttg ctg ctg ctg ctc ccc ttg gcc ttc gtg 48  
 Met Cys Arg Leu Arg Val Leu Leu Leu Leu Leu Pro Leu Ala Phe Val  
 1 5 10 15

tcc tcc tct gct ctc ccc atc cat gat gtc gac tct cag cag aac acc 96  
 Ser Ser Ser Ala Leu Pro Ile His Asp Val Asp Ser Gln Gln Asn Thr  
 20 25 30

tcc ggg ttc ctg ggc ctt cag agg ctt ctc caa agc ttt agt cga ctg 144  
 Ser Gly Phe Leu Gly Leu Gln Arg Leu Leu Gln Ser Phe Ser Arg Leu  
 35 40 45

ttc cta aaa aat gac ctg cta cga gac ctg gac aac ttc ttc tcc tcc	192
Phe Leu Lys Asn Asp Leu Leu Arg Asp Leu Asp Asn Phe Phe Ser Ser	
50 55 60	
ccc atg gac ttc cga gac ctt cct agg aac ttc cat cag gaa gag aac	240
Pro Met Asp Phe Arg Asp Leu Pro Arg Asn Phe His Gln Glu Glu Asn	
65 70 75 80	
cag gag cac aga atg ggc aac cat acc ctc tcc agc cac cta cag ata	288
Gln Glu His Arg Met Gly Asn His Thr Leu Ser Ser His Leu Gln Ile	
85 90 95	
gac aag gtg act gac aac cag aca ggg gag gtg cac atc tcg gag aaa	336
Asp Lys Val Thr Asp Asn Gln Thr Gly Glu Val His Ile Ser Glu Lys	
100 105 110	
gtc gag gcc tcc att gag cca gaa cgg aac ccg gaa ggg gac tgg aag	384
Val Glu Ala Ser Ile Glu Pro Glu Arg Asn Pro Glu Gly Asp Trp Lys	
115 120 125	
gtt ccc aaa gta gaa gca aaa gag ccc ccg gtg cct gtg cag aag gtc	432
Val Pro Lys Val Glu Ala Lys Glu Pro Pro Val Pro Val Gln Lys Val	
130 135 140	
acc gac agc ttg cac cca gag ccc cgg cag gtg gct ttc tgg atc atg	480
Thr Asp Ser Leu His Pro Glu Pro Arg Gln Val Ala Phe Trp Ile Met	
145 150 155 160	
aag atg cca agg cgg agg acc cag ccc gat gtc cag gat gga ggc cgc	528
Lys Met Pro Arg Arg Arg Thr Gln Pro Asp Val Gln Asp Gly Gly Arg	
165 170 175	
tgg ctc ata gaa aag cga cat cgc atg cag gcc atc cgg gat ggg ctc	576
Trp Leu Ile Glu Lys Arg His Arg Met Gln Ala Ile Arg Asp Gly Leu	
180 185 190	
cgt gga ggc gcc cgt gag gac agc ctg gag gat ggg gtc cat atc ccc	624
Arg Gly Gly Ala Arg Glu Asp Ser Leu Glu Asp Gly Val His Ile Pro	
195 200 205	
caa cac gcc aag ctg cct gtc aga aag aca cac ttt,ctc tac atc ctc	672
Gln His Ala Lys Leu Pro Val Arg Lys Thr His Phe Leu Tyr Ile Leu	
210 215 220	
agg cca tcc caa cag ctg	690
Arg Pro Ser Gln Gln Leu	
225 230	

<210> 29

<211> 51

<212> PRT

<213> Artificial Sequence

<220>

<223> Xaa at positions

3-5,7,9-15,18,20-22,24-27,29,31,33,34,36-39,42,44,  
45, and 47-50 may be any amino acid

<220>

<223> Description of Artificial Sequence: consensus sequence

<400> 29

Leu Pro Xaa Xaa Xaa His Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly  
1 5 10 15

Asn Xaa Thr Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Lys Xaa Thr Xaa Asn  
20 25 30

Xaa Xaa Gly Xaa Xaa Xaa Xaa Ser Glu Xaa Val Xaa Xaa Ser Xaa Xaa  
35 40 45

Xaa Xaa Glu  
50

<210> 30

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 30

cagtgagtgc tgtggagacc

20

<210> 31

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

tcttcagtca ggctcctctc

20

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

acctgcaatg tgctgactga g

21

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33  
cacttacagc tgttgggatg

20

<210> 34  
<211> 10  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Xaa at position 1 may be any amino acid

<400> 34  
Xaa Val Leu Asp Phe Asn Asn Ile Arg Ser  
1 5 10

<210> 35  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 35  
Ser Gln Gly Arg Lys Gly Gln Glu Gly Ser  
1 5 10

<210> 36  
<211> 272  
<212> PRT  
<213> Mus musculus

<400> 36  
Met Met Val Val Cys Ala Pro Ala Ala Val Arg Phe Leu Ala Val Phe  
1 5 10 15  
Thr Met Met Ala Leu Cys Ser Leu Pro Leu Leu Gly Ala Ser Ala Thr  
20 25 30  
Leu Asn Ser Val Leu Ile Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro  
35 40 45  
Pro Leu Gly Gly Ala Gly Gly Gln Pro Gly Ser Ala Val Ser Val Ala  
50 55 60  
Pro Gly Val Leu Tyr Glu Gly Gly Asn Lys Tyr Gln Thr Leu Asp Asn  
65 70 75 80  
Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Ser Asp Glu  
85 90 95  
Tyr Cys Ser Ser Pro Ser Arg Gly Ala Ala Gly Val Gly Gly Val Gln  
100 105 110  
Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Thr His Ala  
115 120 125  
Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Met Pro Ser  
130 135 140

Asp His Ser His Phe Pro Arg Gly Glu Ile Glu Glu Ser Ile Ile Glu  
145 150 155 160  
Asn Leu Gly Asn Asp His Asn Ala Ala Ala Gly Asp Gly Tyr Pro Arg  
165 170 175  
Arg Thr Thr Leu Thr Ser Lys Ile Tyr His Thr Lys Gly Gln Glu Gly  
180 185 190  
Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ala Gly Leu Cys Cys Ala  
195 200 205  
Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Lys Glu Gly Gln  
210 215 220  
Val Cys Thr Lys His Lys Arg Lys Gly Ser His Gly Leu Glu Ile Phe  
225 230 235 240  
Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ala Cys Arg Ile Gln Lys Asp  
245 250 255  
His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265 270

<210> 37  
<211> 259  
<212> PRT  
<213> *Xenopus laevis*

<400> 37  
Met Gly Ser Asn Met Phe Pro Val Pro Leu Ile Val Phe Trp Gly Phe  
1 5 10 15  
Ile Leu Asp Gly Ala Leu Gly Phe Val Met Met Thr Asn Ser Asn Ser  
20 25 30  
Ile Lys Asn Val Pro Ala Ala Pro Ala Gly Gln Pro Ile Gly Tyr Tyr  
35 40 45  
Pro Val Ser Val Ser Pro Asp Ser Leu Tyr Asp Ile Ala Asn Lys Tyr  
50 55 60  
Gln Pro Leu Asp Ala Tyr Pro Leu Tyr Ser Cys Thr Glu Asp Asp Asp  
65 70 75 80  
Cys Ala Leu Asp Glu Phe Cys His Ser Ser Arg Asn Gly Asn Ser Leu  
85 90 95  
Val Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg Cys Leu Arg Asp Ala  
100 105 110  
Met Cys Cys Thr Gly Asn Tyr Cys Ser Asn Gly Ile Cys Val Pro Val  
115 120 125  
Glu Gln Asp Gln Glu Arg Phe Gln His Gln Gly Tyr Leu Glu Glu Thr  
130 135 140  
Ile Leu Glu Asn Tyr Asn Asn Ala Asp His Ala Thr Met Asp Thr His  
145 150 155 160

Ser Lys Leu Thr Thr Ser Pro Ser Gly Met Gln Pro Phe Lys Gly Arg  
165 170 175

Asp Gly Asp Val Cys Leu Arg Ser Thr Asp Cys Ala Pro Gly Leu Cys  
180 185 190

Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Asp Glu  
195 200 205

Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu Glu  
210 215 220

Ile Phe Gln Arg Cys His Cys Gly Ala Gly Leu Ser Cys Arg Leu Gln  
225 230 235 240

Lys Gly Glu Phe Thr Thr Val Pro Lys Thr Ser Arg Leu His Thr Cys  
245 250 255

Gln Arg His

<210> 38  
<211> 350  
<212> PRT  
<213> Gallus gallus

<400> 38  
Met Arg Arg Gly Glu Gly Pro Ala Pro Arg Arg Arg Trp Leu Leu Leu  
1 5 10 15

Leu Ala Val Leu Ala Ala Leu Cys Cys Ala Ala Ala Gly Ser Gly Gly  
20 25 30

Arg Arg Arg Ala Ala Ser Leu Gly Glu Met Leu Arg Glu Val Glu Ala  
35 40 45

Leu Met Glu Asp Thr Gln His Lys Leu Arg Asn Ala Val Gln Glu Met  
50 55 60

Glu Ala Glu Glu Glu Gly Ala Lys Lys Leu Ser Glu Val Asn Phe Glu  
65 70 75 80

Asn Leu Pro Pro Thr Tyr His Asn Glu Ser Asn Thr Glu Thr Arg Ile  
85 90 95

Gly Asn Lys Thr Val Gln Thr His Gln Glu Ile Asp Lys Val Thr Asp  
100 105 110

Asn Arg Thr Gly Ser Thr Ile Phe Ser Glu Thr Ile Ile Thr Ser Ile  
115 120 125

Lys Gly Gly Glu Asn Lys Arg Asn His Glu Cys Ile Ile Asp Glu Asp  
130 135 140

Cys Glu Thr Gly Lys Tyr Cys Gln Phe Ser Thr Phe Glu Tyr Lys Cys  
145 150 155 160

Gln Pro Cys Lys Thr Gln His Thr His Cys Ser Arg Asp Val Glu Cys  
165 170 175

Cys Gly Asp Gln Leu Cys Val Trp Gly Glu Cys Arg Lys Ala Thr Ser  
180 185 190

Arg Gly Glu Asn Gly Thr Ile Cys Glu Asn Gln His Asp Cys Asn Pro  
195 200 205

Gly Thr Cys Cys Ala Phe Gln Lys Glu Leu Leu Phe Pro Val Cys Thr  
210 215 220

Pro Leu Pro Glu Glu Gly Glu Pro Cys His Asp Pro Ser Asn Arg Leu  
225 230 235 240

Leu Asn Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Val Leu Glu Arg  
245 250 255

Cys Pro Cys Ala Ser Gly Leu Ile Cys Gln Pro Gln Ser Ser His Ser  
260 265 270

Thr Thr Ser Val Cys Glu Leu Ser Ser Asn Glu Thr Arg Lys Asn Glu  
275 280 285

Lys Glu Asp Pro Leu Asn Met Asp Glu Met Pro Phe Ile Ser Leu Ile  
290 295 300

Pro Arg Asp Ile Leu Ser Asp Tyr Glu Glu Ser Ser Val Ile Gln Glu  
305 310 315 320

Val Arg Lys Glu Leu Glu Ser Leu Glu Asp Gln Ala Gly Val Lys Ser  
325 330 335

Glu His Asp Pro Ala His Asp Leu Phe Leu Gly Asp Glu Ile  
340 345 350

*a1*  
*Cont*

